

#10 1644



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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/752,514A

DATE: 05/15/2002

TIME: 16:21:47

Input Set : A:\KLINEFELTER1C.txt

Output Set: N:\CRF3\05152002\I752514A.raw

3 <110> APPLICANT: KLINEFELTER, Gary  
 5 <120> TITLE OF INVENTION: METHOD FOR EVALUATING AND AFFECTING MALE FERTILITY  
 7 <130> FILE REFERENCE: KLINEFELTER=1C  
 9 <140> CURRENT APPLICATION NUMBER: 09/752,514A  
 10 <141> CURRENT FILING DATE: 2001-01-03  
 12 <150> PRIOR APPLICATION NUMBER: US 09/123,492  
 13 <151> PRIOR FILING DATE: 1998-07-28  
 15 <150> PRIOR APPLICATION NUMBER: PCT/US97/01725  
 16 <151> PRIOR FILING DATE: 1998-01-29  
 18 <150> PRIOR APPLICATION NUMBER: US 08/593,677  
 19 <151> PRIOR FILING DATE: 1996-01-29  
 21 <150> PRIOR APPLICATION NUMBER: US 60/082,753  
 22 <151> PRIOR FILING DATE: 1998-04-23  
 24 <160> NUMBER OF SEQ ID NOS: 4  
 26 <170> SOFTWARE: PatentIn version 3.1  
 28 <210> SEQ ID NO: 1  
 29 <211> LENGTH: 189  
 30 <212> TYPE: PRT  
 31 <213> ORGANISM: Homo sapiens  
 33 <400> SEQUENCE: 1  
 35 Met Ala Ser Lys Arg Ala Leu Val Ile Leu Ala Lys Gly Ala Glu Glu  
 36 1 5 10 15  
 39 Met Glu Thr Val Ile Pro Val Asp Val Met Arg Arg Ala Gly Ile Lys  
 40 20 25 30  
 43 Val Thr Val Ala Gly Leu Ala Gly Lys Asp Pro Val Gln Cys Ser Arg  
 44 35 40 45  
 47 Asp Val Val Ile Cys Pro Asp Ala Ser Leu Glu Asp Ala Lys Lys Glu  
 48 50 55 60  
 51 Gly Pro Tyr Asp Val Val Leu Pro Gly Gly Asn Leu Gly Ala Gln  
 52 65 70 75 80  
 55 Asn Leu Ser Glu Ser Ala Ala Val Lys Glu Ile Leu Lys Glu Gln Glu  
 56 85 90 95  
 59 Asn Arg Lys Gly Leu Ile Ala Ala Ile Cys Ala Gly Pro Thr Ala Leu  
 60 100 105 110  
 63 Leu Ala His Glu Ile Gly Cys Gly Ser Lys Val Thr Thr His Pro Leu  
 64 115 120 125  
 67 Ala Lys Asp Lys Met Met Asn Gly Gly His Tyr Thr Tyr Ser Glu Asn  
 68 130 135 140  
 71 Arg Val Glu Lys Asp Gly Leu Ile Leu Thr Ser Arg Gly Pro Gly Thr  
 72 145 150 155 160  
 75 Ser Phe Glu Phe Ala Leu Ala Ile Val Glu Ala Leu Asn Gly Lys Glu  
 76 165 170 175  
 79 Val Ala Ala Gln Val Lys Ala Pro Leu Val Leu Lys Asp

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80          180          185
83 <210> SEQ ID NO: 2
84 <211> LENGTH: 980
85 <212> TYPE: DNA
86 <213> ORGANISM: Rattus rattus
88 <220> FEATURE:
89 <221> NAME/KEY: CDS
90 <222> LOCATION: (190)..(756)
91 <223> OTHER INFORMATION:
94 <400> SEQUENCE: 2
95 gctgtgcaga gccgtctggc aggggttgacc tcctaaaggg atattccatc tttattaatc      60
97 attagtagtg tggtcagaga cttagcacca ttggtctccc ccaacctggt ccagacattt      120
99 cagcagttta tcggaacagc aacaacagca acaaacctt caaaatttac aagtctttaa      180
101 gaaatagaa atg gca tcc aaa aga gct ctg gtc atc cta gcc aaa gga gca      231
102      Met Ala Ser Lys Arg Ala Leu Val Ile Leu Ala Lys Gly Ala
103      1          5          10
105 gag gag atg gag aca gtg att cct gtg gac atc atg cgg cga gct ggg      279
106 Glu Glu Met Glu Thr Val Ile Pro Val Asp Ile Met Arg Arg Ala Gly
107 15          20          25          30
109 att aaa gtc acc gtt gca ggc ttg gct ggg aag gac ccc gtg cag tgt      327
110 Ile Lys Val Thr Val Ala Gly Leu Ala Gly Lys Asp Pro Val Gln Cys
111          35          40          45
113 agc cgt gat gta gtg att tgt ccg gat acc agt ctg gaa gaa gca aaa      375
114 Ser Arg Asp Val Val Ile Cys Pro Asp Thr Ser Leu Glu Glu Ala Lys
115          50          55          60
117 aca cag gga cca tac gat gtg gtt gtt ctt cca gga gga aat ctg ggt      423
118 Thr Gln Gly Pro Tyr Asp Val Val Val Leu Pro Gly Gly Asn Leu Gly
119          65          70          75
121 gca cag aac tta tct gag tcg gct ttg gtg aag gag atc ctc aag gag      471
122 Ala Gln Asn Leu Ser Glu Ser Ala Leu Val Lys Glu Ile Leu Lys Glu
123      80          85          90
125 cag gag aac agg aag ggc ctc ata gct gcc atc tgt gcg ggt cct acg      519
126 Gln Glu Asn Arg Lys Gly Leu Ile Ala Ala Ile Cys Ala Gly Pro Thr
127 95          100          105          110
129 gcc ctg ctg gct cac gaa gta ggc ttt gga tgc aag gtt aca tcg cac      567
130 Ala Leu Leu Ala His Glu Val Gly Phe Gly Cys Lys Val Thr Ser His
131          115          120          125
133 cca ttg gct aag gac aaa atg atg aac ggc agt cac tac agc tac tca      615
134 Pro Leu Ala Lys Asp Lys Met Met Asn Gly Ser His Tyr Ser Tyr Ser
135          130          135          140
137 gag agc cgt gtg gag aag gac ggc ctc atc ctc acc agc cgt ggg cct      663
138 Glu Ser Arg Val Glu Lys Asp Gly Leu Ile Leu Thr Ser Arg Gly Pro
139          145          150          155
141 ggg acc agc ttc gag ttt gcg ctg gcc att gtg gag gca ctc agt ggc      711
142 Gly Thr Ser Phe Glu Phe Ala Leu Ala Ile Val Glu Ala Leu Ser Gly
143          160          165          170
145 aag gac atg gct aac caa gtg aag gcc ccg ctt gtt ctc aaa gac      756
146 Lys Asp Met Ala Asn Gln Val Lys Ala Pro Leu Val Leu Lys Asp
147 175          180          185

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149 tagagagccc aagccctgga ccctggaccc ccaggctgag caggcattgg aagcccacta      816
151 gtgtgtccac agcccagtga acctggcatt ggaagcccac tagtgtgtcc acagcccagt      876
153 gaacctcagg aactaacgtg tgaagtagcc cgctgctcag gaatctcgcc ctggctctgt      936
155 actattctga gccttgctag tagaataaac agttccccaa gctc                        980

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158 &lt;210&gt; SEQ ID NO: 3

159 &lt;211&gt; LENGTH: 189

160 &lt;212&gt; TYPE: PRT

161 &lt;213&gt; ORGANISM: Rattus rattus

163 &lt;400&gt; SEQUENCE: 3

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165 Met Ala Ser Lys Arg Ala Leu Val Ile Leu Ala Lys Gly Ala Glu Glu
166 1          5          10          15
169 Met Glu Thr Val Ile Pro Val Asp Ile Met Arg Arg Ala Gly Ile Lys
170          20          25          30
173 Val Thr Val Ala Gly Leu Ala Gly Lys Asp Pro Val Gln Cys Ser Arg
174          35          40          45
177 Asp Val Val Ile Cys Pro Asp Thr Ser Leu Glu Glu Ala Lys Thr Gln
178          50          55          60
181 Gly Pro Tyr Asp Val Val Val Leu Pro Gly Gly Asn Leu Gly Ala Gln
182 65          70          75          80
185 Asn Leu Ser Glu Ser Ala Leu Val Lys Glu Ile Leu Lys Glu Gln Glu
186          85          90          95
189 Asn Arg Lys Gly Leu Ile Ala Ala Ile Cys Ala Gly Pro Thr Ala Leu
190          100         105         110
193 Leu Ala His Glu Val Gly Phe Gly Cys Lys Val Thr Ser His Pro Leu
194          115         120         125
197 Ala Lys Asp Lys Met Met Asn Gly Ser His Tyr Ser Tyr Ser Glu Ser
198          130         135         140
201 Arg Val Glu Lys Asp Gly Leu Ile Leu Thr Ser Arg Gly Pro Gly Thr
202 145         150         155         160
205 Ser Phe Glu Phe Ala Leu Ala Ile Val Glu Ala Leu Ser Gly Lys Asp
206          165         170         175
209 Met Ala Asn Gln Val Lys Ala Pro Leu Val Leu Lys Asp
210          180         185

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213 &lt;210&gt; SEQ ID NO: 4

214 &lt;211&gt; LENGTH: 842

215 &lt;212&gt; TYPE: DNA

216 &lt;213&gt; ORGANISM: Rattus rattus

218 &lt;220&gt; FEATURE:

219 &lt;221&gt; NAME/KEY: CDS

220 &lt;222&gt; LOCATION: (52)..(618)

221 &lt;223&gt; OTHER INFORMATION:

224 &lt;400&gt; SEQUENCE: 4

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225 tggcttcgcg tgggtggagg aggcgcggct gcaggctctt aagaaataga a atg gca      57
226                               Met Ala
227                               1
229 tcc aaa aga gct ctg gtc atc cta gcc aaa gga gca gag gag atg gag      105
230 Ser Lys Arg Ala Leu Val Ile Leu Ala Lys Gly Ala Glu Glu Met Glu
231 5          10          15
233 aca gtg att cct gtg gac atc atg cgg cga gct ggg att aaa gtc acc      153

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234	Thr	Val	Ile	Pro	Val	Asp	Ile	Met	Arg	Arg	Ala	Gly	Ile	Lys	Val	Thr	
235		20					25					30					
237	gtt	gca	ggc	ttg	gct	ggg	aag	gac	ccc	gtg	cag	tgt	agc	cgt	gat	gta	201
238	Val	Ala	Gly	Leu	Ala	Gly	Lys	Asp	Pro	Val	Gln	Cys	Ser	Arg	Asp	Val	
239	35					40				45					50		
241	gtg	att	tgt	ccg	gat	acc	agt	ctg	gaa	gaa	gca	aaa	aca	cag	gga	cca	249
242	Val	Ile	Cys	Pro	Asp	Thr	Ser	Leu	Glu	Glu	Ala	Lys	Thr	Gln	Gly	Pro	
243					55				60					65			
245	tac	gat	gtg	gtt	gtt	ctt	cca	gga	gga	aat	ctg	ggt	gca	cag	aac	tta	297
246	Tyr	Asp	Val	Val	Val	Leu	Pro	Gly	Gly	Asn	Leu	Gly	Ala	Gln	Asn	Leu	
247			70					75				80					
249	tct	gag	tcg	gct	ttg	gtg	aag	gag	atc	ctc	aag	gag	cag	gag	aac	agg	345
250	Ser	Glu	Ser	Ala	Leu	Val	Lys	Glu	Ile	Leu	Lys	Glu	Gln	Glu	Asn	Arg	
251			85				90					95					
253	aag	ggc	ctc	ata	gct	gcc	atc	tgt	gcg	ggt	cct	acg	gcc	ctg	ctg	gct	393
254	Lys	Gly	Leu	Ile	Ala	Ala	Ile	Cys	Ala	Gly	Pro	Thr	Ala	Leu	Leu	Ala	
255		100				105					110						
257	cac	gaa	gta	ggc	ttt	gga	tgc	aag	gtt	aca	tcg	cac	cca	ttg	gct	aag	441
258	His	Glu	Val	Gly	Phe	Gly	Cys	Lys	Val	Thr	Ser	His	Pro	Leu	Ala	Lys	
259	115				120				125					130			
261	gac	aaa	atg	atg	aac	ggc	agt	cac	tac	agc	tac	tca	gag	agc	cgt	gtg	489
262	Asp	Lys	Met	Met	Asn	Gly	Ser	His	Tyr	Ser	Tyr	Ser	Glu	Ser	Arg	Val	
263				135				140					145				
265	gag	aag	gac	ggc	ctc	atc	ctc	acc	agc	cgt	ggg	cct	ggg	acc	agc	ttc	537
266	Glu	Lys	Asp	Gly	Leu	Ile	Leu	Thr	Ser	Arg	Gly	Pro	Gly	Thr	Ser	Phe	
267			150				155				160						
269	gag	ttt	gcg	ctg	gcc	att	gtg	gag	gca	ctc	agt	ggc	aag	gac	atg	gct	585
270	Glu	Phe	Ala	Leu	Ala	Ile	Val	Glu	Ala	Leu	Ser	Gly	Lys	Asp	Met	Ala	
271			165				170				175						
273	aac	caa	gtg	aag	gcc	ccg	ctt	gtt	ctc	aaa	gac	tagagagccc	aagccctgga				638
274	Asn	Gln	Val	Lys	Ala	Pro	Leu	Val	Leu	Lys	Asp						
275		180				185											
277	ccctggaccc	ccaggctgag	caggcattgg	aagcccacta	gtgtgtccac	agcccagtga											698
279	acctggcatt	ggaagcccac	tagtgtgtcc	acagcccagt	gaacctcagg	aactaacgtg											758
281	tgaagtagcc	cgctgctcag	gaatctcgcc	ctggctctgt	actattctga	gccttgctag											818
283	tagaataaac	agttcccca	gctc														842

VERIFICATION SUMMARY

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Input Set : A:\KLINEFELTER1C.txt

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